|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table S5.Functional categories of the differentially expressed transcripts in *13 kDa prolamin*-knockout lines in comparison with WT | | | | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |
| BIN Codea | Annotation | *1a-8-1 vs* Ilmi | | | | *2a-2-1 vs* Ilmi | | | | *4b-9-7 vs* Ilmi | | | | *8b-3-9 vs* Ilmi | | | | Total number of non-redundant genes | | | |
| Up | | Down | | Up | | Down | | Up | | Down | | Up | | Down | | Up | | Down | |
| No. | % | No. | % | No. | % | No. | % | No. | % | No. | % | No. | % | No. | % | No. | % | No. | % |
| 1 | Photosyntheisis | 1 | 0.37% | 4 | 3.25% | 0 | 0.00% | 6 | 3.37% | 0 | 0.00% | 4 | 4.00% | 4 | 2.29% | 5 | 2.28% | 4 | 1.23% | 12 | 5.24% |
| 2/3/4/7/8b | Carbohydrate metabolism-related BINs | 4 | 1.49% | 1 | 0.81% | 2 | 1.03% | 2 | 1.12% | 0 | 0.00% | 0 | 0.00% | 0 | 0.00% | 7 | 3.20% | 5 | 1.53% | 7 | 3.06% |
| 9 | Mitochondrial electron transport/ATP synthesis | 12 | 4.48% | 0 | 0.00% | 1 | 0.52% | 1 | 0.56% | 0 | 0.00% | 0 | 0.00% | 2 | 1.14% | 2 | 0.91% | 14 | 4.29% | 3 | 1.31% |
| 10 | Cell wall | 5 | 1.87% | 1 | 0.81% | 3 | 1.55% | 1 | 0.56% | 1 | 0.85% | 1 | 1.00% | 0 | 0.00% | 1 | 0.46% | 9 | 2.76% | 1 | 0.44% |
| 11 | Lipid metabolism | 0 | 0.00% | 2 | 1.63% | 4 | 2.06% | 2 | 1.12% | 0 | 0.00% | 1 | 1.00% | 0 | 0.00% | 1 | 0.46% | 4 | 1.23% | 5 | 2.18% |
| 12/14/16/18/21/23/24c | Other metabolism-related BINs | 1 | 0.37% | 2 | 1.63% | 2 | 1.03% | 7 | 3.93% | 2 | 1.71% | 0 | 0.00% | 2 | 1.14% | 7 | 3.20% | 5 | 1.53% | 11 | 4.80% |
| 13 | Amino acid metabolism | 1 | 0.37% | 0 | 0.00% | 1 | 0.52% | 1 | 0.56% | 0 | 0.00% | 0 | 0.00% | 3 | 1.71% | 2 | 0.91% | 4 | 1.23% | 2 | 0.87% |
| 17 | Hormone metabolism | 2 | 0.75% | 2 | 1.63% | 4 | 2.06% | 1 | 0.56% | 0 | 0.00% | 1 | 1.00% | 4 | 2.29% | 1 | 0.46% | 5 | 1.53% | 3 | 1.31% |
| 20 | Stress | 4 | 1.49% | 3 | 2.44% | 11 | 5.67% | 2 | 1.12% | 11 | 9.40% | 0 | 0.00% | 10 | 5.71% | 5 | 2.28% | 23 | 7.06% | 7 | 3.06% |
| 26 | Miscellaneous | 13 | 4.85% | 5 | 4.07% | 4 | 2.06% | 7 | 3.93% | 4 | 3.42% | 3 | 3.00% | 4 | 2.29% | 8 | 3.65% | 20 | 6.13% | 15 | 6.55% |
| 27.1 | RNA.processing | 40 | 14.93% | 29 | 23.58% | 35 | 18.04% | 37 | 20.79% | 25 | 21.37% | 27 | 27.00% | 31 | 17.71% | 30 | 13.70% | 83 | 25.46% | 69 | 30.13% |
| 27.2/3 | RNA.transcription and RNA.regulation of transcription | 5 | 1.87% | 2 | 1.63% | 12 | 6.19% | 5 | 2.81% | 4 | 3.42% | 2 | 2.00% | 7 | 4.00% | 12 | 5.48% | 20 | 6.13% | 17 | 7.42% |
| 28 | DNA synthesis and repair | 0 | 0.00% | 1 | 0.81% | 0 | 0.00% | 1 | 0.56% | 0 | 0.00% | 0 | 0.00% | 1 | 0.57% | 2 | 0.91% | 1 | 0.31% | 3 | 1.31% |
| 29.3/4/5/6d | Protein activity regulation-related BINs | 7 | 2.61% | 6 | 4.88% | 6 | 3.09% | 9 | 5.06% | 3 | 2.56% | 3 | 3.00% | 2 | 1.14% | 9 | 4.11% | 16 | 4.91% | 18 | 7.86% |
| 29.2.1/4 | Protein synthesis-ribosome and elongation | 2 | 0.75% | 2 | 1.63% | 0 | 0.00% | 1 | 0.56% | 1 | 0.85% | 1 | 1.00% | 1 | 0.57% | 2 | 0.91% | 4 | 1.23% | 4 | 1.75% |
| 29.2.6 | Protein synthesis-ribosomal RNA | 36 | 13.43% | 0 | 0.00% | 0 | 0.00% | 0 | 0.00% | 2 | 1.71% | 1 | 1.00% | 3 | 1.71% | 0 | 0.00% | 36 | 11.04% | 1 | 0.44% |
| 29.2.7 | Protein synthesis\_transfer RNA | 8 | 2.99% | 8 | 6.50% | 4 | 2.06% | 7 | 3.93% | 2 | 1.71% | 13 | 13.00% | 4 | 2.29% | 22 | 10.05% | 15 | 4.60% | 25 | 10.92% |
| 30 | Signalling | 6 | 2.24% | 0 | 0.00% | 3 | 1.55% | 1 | 0.56% | 2 | 1.71% | 0 | 0.00% | 3 | 1.71% | 4 | 1.83% | 10 | 3.07% | 4 | 1.75% |
| 31 | Cell organization | 1 | 0.37% | 1 | 0.81% | 3 | 1.55% | 2 | 1.12% | 1 | 0.85% | 2 | 2.00% | 3 | 1.71% | 3 | 1.37% | 6 | 1.84% | 4 | 1.75% |
| 33 | Development | 24 | 8.96% | 3 | 2.44% | 9 | 4.64% | 2 | 1.12% | 4 | 3.42% | 1 | 1.00% | 6 | 3.43% | 3 | 1.37% | 30 | 9.20% | 8 | 3.49% |
| 34 | Transport | 8 | 2.99% | 1 | 0.81% | 4 | 2.06% | 4 | 2.25% | 1 | 0.85% | 1 | 1.00% | 4 | 2.29% | 7 | 3.20% | 12 | 3.68% | 10 | 4.37% |
| 35 | Unknown | 88 | 32.84% | 50 | 40.65% | 86 | 44.33% | 79 | 44.38% | 54 | 46.15% | 39 | 39.00% | 81 | 46.29% | 86 | 39.27% | 214 |  | 174 |  |
| Total |  | 268 | 100.00% | 123 | 100.00% | 194 | 100.00% | 178 | 100.00% | 117 | 100.00% | 100 | 100.00% | 175 | 100.00% | 219 | 100.00% | 540 | 100.00% | 403 | 100.00% |
| a BIN codes of genes were produced according to MapMan classification using the MapCave tool (http://mapman.gabipd.org/web/guest/mapcave). | | | | | | | | | | | | | | |  |  |  |  |  |  |  |
| b BIN 2/3/4/7/8 is carbohydrate metabolism-related BINs: major carbohydrates (BIN 2), minor carbohydrates (BIN 3), glycolysis (BIN 4), OPP cycle (BIN 7), and TCA/organic acid transformation (BIN 8) | | | | | | | | | | | | | | |  |  |  |  |  |  |  |
| c BIN 12/14/16/18/21/23/24 is the other metabolism-related BINs: nitrogen assimilation (BIN 12), S-assimilation (BIN 14), secondary metabolism (BIN 16), cofactor/vitamin synthesis (BIN 18), redox (BIN 21), nucleotide metabolism (BIN 23), biodegradation of xenobiotics (BIN 24) | | | | | | | | | | | | | | | | | |  |  |  |  |
| d BIN 29.3/4/5/6 is protein activity regulation-related BINs including protein targeting (BIN 29.3), protein post-translational modification (BIN 29.4), protein degradation (BIN 29.5), and protein folding (BIN 29.6) | | | | | | | | | | | | | | |  |  |  |  |  |  |  |